SEQUENCE LISTING

<110> Saris, Christiaan M.
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      Mu, Sharon X.
      Xia, Min
      Bass, Michael B.
      Craveiro, Roger

<120> Interleukin-1 Receptor Antagonist-Related Molecules and
      Uses Thereof

<130> 00-1213

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<150> 60/170,191
<151> 1999-12-10

<150> 60/188,053
<151> 2000-03-09

<150> 60/194,521
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<170> PatentIn Ver. 2.0

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    Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
      1   5   10   15

gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat   156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                20   25   30

cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac   204
Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
            35   40   45

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aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga    252
Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
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ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta    300
Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
         65                  70                  75

cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag    348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
      80                  85                  90                  95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg    396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                    100                 105                 110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag    444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
                115                 120                 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt    492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
            130                 135                 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt    542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
        145                 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag 782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat 842

gcaggtgttt ttagaaggtg gaaaagccaa gggaacggat tctcctctag agtctccgga 902

aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

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2

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        Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg
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        Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
             50                  55                  60

        Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
        65                  70                  75                      80

        Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
                         85                  90                  95

        Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
                     100                 105                 110

        Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
                 115                 120                 125

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            Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
              1               5                  10                      15

        gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat    156
        Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                         20                  25                  30

        cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt cct aac    204
        Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn
                         35                  40                  45

        aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc cag gga    252
        Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
                     50                  55                  60

        ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta    300
        Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
                 65                  70                  75
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3

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cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag    348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
 80              85              90                      95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg    396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                100             105             110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag    444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
            115             120             125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt    492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
        130             135             140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt      542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
        145             150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag 782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat 842

gcaggtgttt ttagaaggtg aaaagccaa  gggaacggat tctcctctag agtctccgga 902

aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

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            20                  25                  30

Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn Arg
        35                  40                  45

Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
    50                  55                  60

Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
65                  70                  75                  80
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4

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Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
                85                      90                      95

Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
            100                     105                 110

Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
        115                     120                 125

Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr
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Lys Phe Tyr Phe Glu Gln Ser Trp
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Met Val Leu Ser Gly Ala Leu Cys Phe Arg Glu Asp Gln Thr Pro Leu
 1               5                  10                  15

att gca gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa      153
Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
            20                  25                  30

tat gca gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg      201
Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
        35                  40                  45

gga gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt      249
Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
    50                  55                  60

cct aac aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc      297
Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
 65                 70                  75                  80

cag gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct      345
Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
            85                  90                  95

tcc cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt      393
Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly
            100                 105                 110
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gaa gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc    441
Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
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ttc agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg    489
Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
    130                 135                 140

gca gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca    537
Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser
145                 150                 155                 160

gcc cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga         583
Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
                165                 170

aactgcgttt tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg 643

cagaataatg tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac 703

catacatgtc caaagaggtt ttgcaaatgt gattatgtta a                      744


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Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
            20                  25                  30

Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
        35                  40                  45

Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
    50                  55                  60

Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
65                  70                  75                  80

Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
                85                  90                  95

Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly
                100                 105                 110

Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
        115                 120                 125

Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
    130                 135                 140

Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser
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6

Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
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<213> Homo sapiens

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            20   25   30

Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile
        35   40   45

Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala
    50   55   60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro
65   70   75   80

Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe
                85   90   95

Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala
            100   105   110

Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp
        115   120   125

Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala
    130   135   140

Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met
145   150   155   160

Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu
            165   170   175

Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp
            180   185   190

Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys
        195   200   205

Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn
    210   215   220

Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr
225   230   235   240

Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly
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Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser
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Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
                20   25   30

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
            35   40   45

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
        50   55   60

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
  65   70   75   80

Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
                85   90   95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
            100   105   110

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
        115   120   125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
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Asp Phe Thr Met Gln Phe Val Ser Ser
145   150

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Ser Lys Ile Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe

8

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    Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
         50                  55                  60

    Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala
     65                  70                  75                  80

    Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys
                     85                  90                  95

    Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp
                 100                 105                 110

    Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser
             115                 120                 125

    Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
         130                 135                 140

    Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn
    145                 150                 155                 160

    Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp
                 165                 170                 175

    Glu


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                 20                  25                  30

    Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
             35                  40                  45

    Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
         50                  55                  60

    Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
     65                  70                  75                  80

    Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
                     85                  90                  95

    Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
                 100                 105                 110
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9

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
        115   120   125

Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
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Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145   150   155

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            20   25   30

Pro Leu Glu Pro Gly Pro Ser Leu Pro Thr Met Asn Phe Val His Thr
        35   40   45

Lys Ile Phe Phe Ala Leu Ala Ser Ser Leu Ser Ser Ala Ser Ala Glu
    50   55   60

Lys Gly Ser Pro Ile Leu Leu Gly Val Ser Lys Gly Glu Phe Cys Leu
  65   70   75   80

Tyr Cys Asp Lys Asp Lys Gly Gln Ser His Pro Ser Leu Gln Leu Lys
                85   90   95

Lys Glu Lys Leu Met Lys Leu Ala Ala Gln Lys Glu Ser Ala Arg Arg
            100   105   110

Pro Phe Ile Phe Tyr Arg Ala Gln Val Gly Ser Trp Asn Met Leu Glu
        115   120   125

Ser Ala Ala His Pro Gly Trp Phe Ile Cys Thr Ser Cys Asn Cys Asn
        130   135   140

Glu Pro Val Gly Val Thr Asp Lys Phe Glu Asn Arg Lys His Ile Glu
145   150   155   160

Phe Ser Phe Gln Pro Val Cys Lys Ala Glu Met Ser Pro Ser Glu Val
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Ser Asp

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10

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              20   25   30

Pro Leu Glu Pro Gly Pro Ser Leu Pro Thr Met Asn Phe Val His Thr
          35   40   45

Ser Pro Lys Val Lys Asn Leu Asn Pro Lys Lys Phe Ser Ile His Asp
      50   55   60

Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu Ile Ala Val
 65   70   75   80

Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile Phe Phe Ala Leu Ala Ser
              85   90   95

Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly Ser Pro Ile Leu Leu Gly
          100   105   110

Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp Lys Gly Gln
      115   120   125

Ser His Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met Lys Leu Ala
      130   135   140

Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr Arg Ala Gln
 145   150   155   160

Val Gly Ser Trp Asn Met Leu Glu Ser Ala Ala His Pro Gly Trp Phe
              165   170   175

Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val Thr Asp Lys
          180   185   190

Phe Glu Asn Arg Lys His Ile Glu Phe Ser Phe Gln Pro Val Cys Lys
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Ala Glu Met Ser Pro Ser Glu Val Ser Asp
      210   215

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Phe Lys Lys Arg Leu Arg Gly Pro Lys Val Lys Asn Leu Asn Pro Lys
              20   25   30

11

Lys Phe Ser Ile His Asp Gln Asp His Lys Val Leu Val Leu Asp Ser
          35   40   45

Gly Asn Leu Ile Ala Val Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile
      50   55   60

Phe Phe Ala Leu Ala Ser Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly
 65   70   75   80

Ser Pro Ile Leu Leu Gly Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys
              85   90   95

Asp Lys Asp Lys Gly Gln Ser His Pro Ser Leu Gln Leu Lys Lys Glu
          100   105   110

Lys Leu Met Lys Leu Ala Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe
          115   120   125

Ile Phe Tyr Arg Ala Gln Val Gly Ser Trp Asn Met Leu Glu Ser Ala
      130   135   140

Ala His Pro Gly Trp Phe Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro
145   150   155   160

Val Gly Val Thr Asp Lys Phe Glu Asn Arg Lys His Ile Glu Phe Ser
              165   170   175

Phe Gln Pro Val Cys Lys Ala Glu Met Ser Pro Ser Glu Val Ser Asp
              180   185   190

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 1   5   10   15

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              20   25   30

Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
          35   40   45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
      50   55   60

Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 65   70   75   80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
              85   90   95

12

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
            100   105   110

Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
            115   120   125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
        130   135   140

Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
145   150   155   160

Thr Ala Phe Glu Leu Asn Ile Asn Asp
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            20   25   30

Pro Ser Ala Leu Thr Leu Ser Pro Val Glu Ala Pro Ala Phe Ser Ala
            35   40   45

Pro Leu Cys Thr Leu Pro Phe Pro Pro Val Cys Lys Pro Ile Thr Gly
        50   55   60

Thr Ile Asn Asp Leu Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn
 65   70   75   80

Leu Val Ala Val Pro Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala
                85   90   95

Val Ile Thr Cys Lys Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp
            100   105   110

Pro Ile Tyr Leu Gly Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu
            115   120   125

Lys Val Gly Glu Gln Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met
        130   135   140

Asp Leu Tyr Gly Gln Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg
145   150   155   160

Ala Lys Thr Gly Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp
                165   170   175

Trp Phe Ile Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser

13

Glu Leu Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
        195   200   205

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<400> 16
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  1   5   10   15

Asp Ile Asn His Arg Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala
            20   25   30

Val Pro Arg Lys Asp Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser
        35   40   45

Cys Arg His Val Glu Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr
    50   55   60

Leu Gly Leu Asn Gly Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly
 65   70   75   80

Asp Gln Pro Thr Leu Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr
                85   90   95

Asn Gln Pro Glu Pro Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser
            100   105   110

Gly Arg Asn Ser Thr Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile
        115   120   125

Ala Val Ser Ser Glu Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu
    130   135   140

Gly Lys Ala Asn Thr Thr Asp Phe Gly Leu Thr Met Leu Phe
145   150   155

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<213> Homo sapiens

<400> 17
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Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
            20   25   30

Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
        35   40   45

Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
    50   55   60

Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
65   70   75   80

Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
                85   90   95

Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
            100   105   110

Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
        115   120   125

Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
    130   135   140

Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
145   150   155

<210> 18
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<213> Human immunodeficiency virus type 1

<400> 18
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<210> 19
<211> 15
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<220>
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      domain derived from HIV tat protein

<400> 19
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  1   5   10   15

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<211> 23
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<220>
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15

Oligonucleotide 2349-98

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<210> 22
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<212> DNA
<213> Artificial Sequence

<220>
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16

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<210> 26
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<210> 27
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<210> 29
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<210> 30
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<220>
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<210> 31
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<210> 32
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<212> DNA
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<223> Description of Artificial Sequence:
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<210> 33
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<213> Artificial Sequence

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<210> 34
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1   5   10   15

caa aag gct ttg tac aca cgg aat ggc cag ctc ctg ctg gga gac cct   96
Gln Lys Ala Leu Tyr Thr Arg Asn Gly Gln Leu Leu Leu Gly Asp Pro
                20   25   30

gat tca gac aat tat agt cca gag aag gtc tgt atc ctt cct aac cga   144
Asp Ser Asp Asn Tyr Ser Pro Glu Lys Val Cys Ile Leu Pro Asn Arg
            35   40   45

ggc cta gac cgc tcc aag gtc ccc atc ttc ctg ggg atg cag gga gga   192
Gly Leu Asp Arg Ser Lys Val Pro Ile Phe Leu Gly Met Gln Gly Gly
        50   55   60

agt tgc tgc ctg gcg tgt gta aag aca aga gag gga cct ctc ctg cag   240
Ser Cys Cys Leu Ala Cys Val Lys Thr Arg Glu Gly Pro Leu Leu Gln
65   70   75   80

ctg gag gat gtg aac atc gag gac cta tac aag gga ggt gaa caa acc   288
Leu Glu Asp Val Asn Ile Glu Asp Leu Tyr Lys Gly Gly Glu Gln Thr
                85   90   95

acc cgt ttc acc ttt ttc cag aga agc ttg gga tct gcc ttc agg ctt   336
Thr Arg Phe Thr Phe Phe Gln Arg Ser Leu Gly Ser Ala Phe Arg Leu
            100   105   110

gag gct gct gcc tgc cct ggc tgg ttt ctc tgt ggc cca gct gag ccc   384
Glu Ala Ala Ala Cys Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro

19

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Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Thr His Thr
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Glu Phe Tyr Phe Glu Met Ser Arg
145                     150
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<210> 36
<211> 152
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<213> Mus musculus

<400> 36
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            20                  25                  30

Asp Ser Asp Asn Tyr Ser Pro Glu Lys Val Cys Ile Leu Pro Asn Arg
            35                  40                  45

Gly Leu Asp Arg Ser Lys Val Pro Ile Phe Leu Gly Met Gln Gly Gly
    50                  55                  60

Ser Cys Cys Leu Ala Cys Val Lys Thr Arg Glu Gly Pro Leu Leu Gln
 65                 70                  75                  80

Leu Glu Asp Val Asn Ile Glu Asp Leu Tyr Lys Gly Gly Glu Gln Thr
                85                  90                  95

Thr Arg Phe Thr Phe Phe Gln Arg Ser Leu Gly Ser Ala Phe Arg Leu
            100                 105                 110

Glu Ala Ala Ala Cys Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
            115                 120                 125

Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Thr His Thr
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Glu Phe Tyr Phe Glu Met Ser Arg
145                 150
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22

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24

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25

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